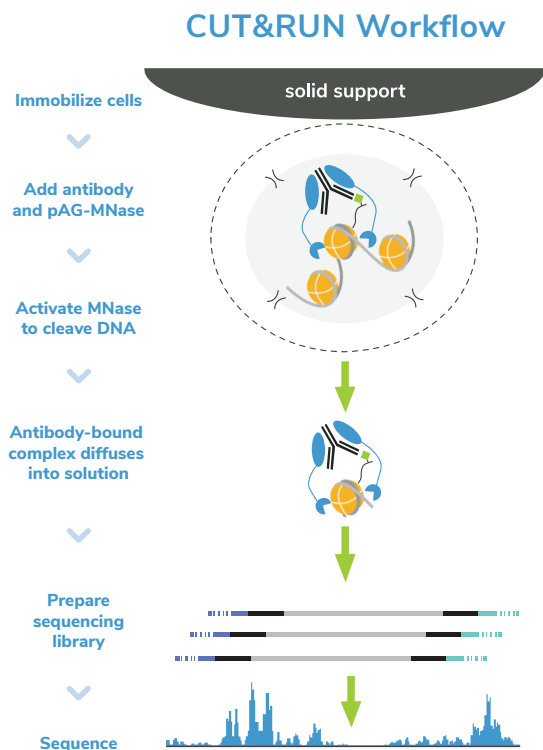


CUTANA™ CUT&RUN Assays For Ultra-Sensitive Genomic Mapping

Cleavage Under Targets & Release Using Nuclease (CUT&RUN) is a breakthrough method for genomic mapping of protein-DNA interactions and histone post-translational modifications (PTMs). For new users, our CUTANA™ CUT&RUN platform provides everything you need to get started, including user-friendly kits, protocols, validated antibodies, and more.



Advantages

- Save 10x in sequencing costs (vs. ChIP-seq)
- Use fewer cells (down to 5k)
- Works with a diversity of targets & sample types
- User-friendly workflow with reproducible results

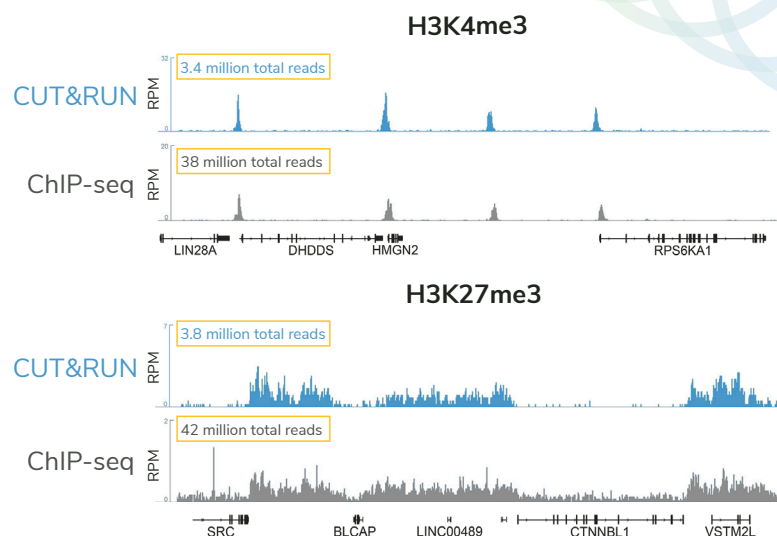


FIGURE 1 CUTANA CUT&RUN outperforms ChIP-seq using fewer sequencing reads.

CUTANA™ CUT&RUN Profiles Diverse Targets

CUT&RUN enables investigation of a wide variety of target classes, including transcription factors, chromatin-interacting proteins, and histone modifications. CUT&RUN also provides access to challenging targets like chromatin remodelers.

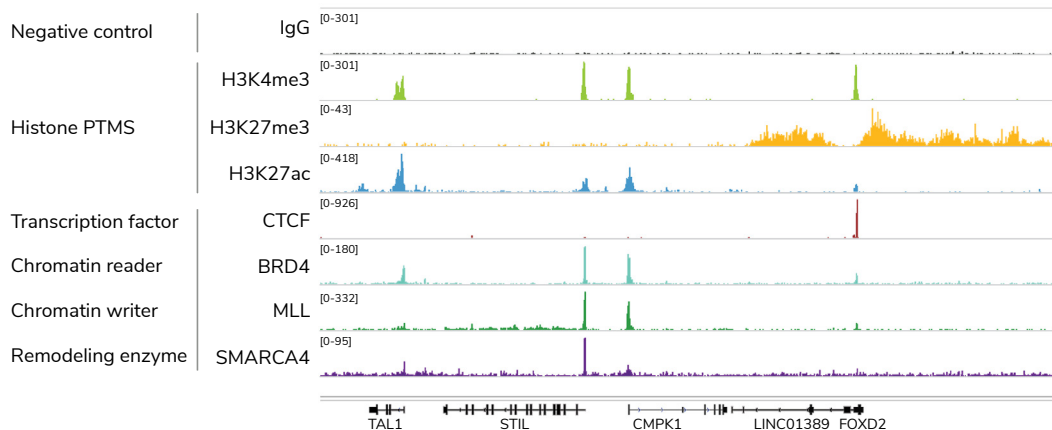
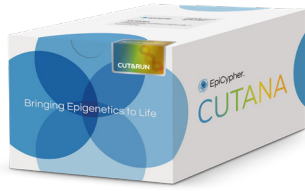


FIGURE 2 Representative genome browser tracks show CUTANA CUT&RUN results using K562 cells. Clear peaks with the expected distribution profile are observed using 3-8 million sequencing reads per sample for a variety of epigenetic targets.

New Users: Where to Start?



CUTANA™ CUT&RUN AND LIBRARY PREP KITS

- Together, our CUT&RUN and Library Prep Kits offer an all-inclusive workflow from cells to sequencing
- Compatible with fresh, frozen, or cross-linked cells or nuclei
- We recommend these kits to start setting up CUT&RUN in your laboratory!

CUTANA™ REAGENTS

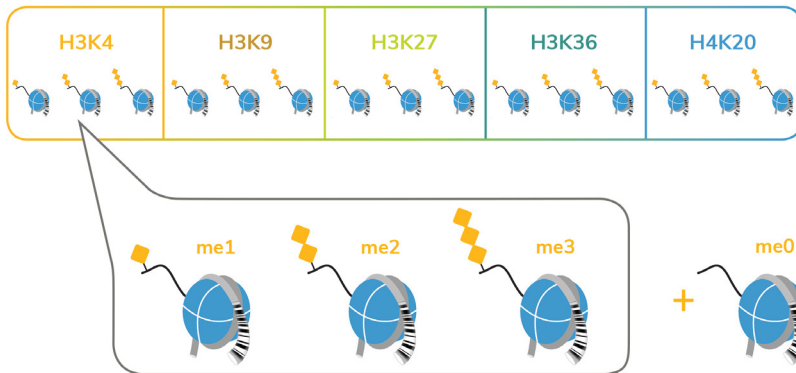
- Design and execute custom CUT&RUN experiments
- Individual components include ConA beads, pAG-MNase, E. coli spike-in DNA, a DNA purification kit, and more
- All reagents tested and validated for our optimized CUTANA™ CUT&RUN workflow

CUTANA™ CUT&RUN ANTIBODIES

- Available for various chromatin targets including histone PTMs, transcription factors, and chromatin remodelers.
- Lot-validated by EpiCypher scientists for robust performance in CUTANA™ CUT&RUN assays.
- Check regularly for new targets!

SNAP Spike-ins: Quantitative Nucleosome Controls for Epigenomics

SNAP Spike-ins use panels of DNA-barcoded nucleosomes carrying widely-studied histone PTMs as quantitative spike-in controls for epigenomics assays. These controls improve assay reliability and enable accurate sample normalization. SNAP Spike-ins are now available for CUT&RUN, CUT&Tag, and ChIP-seq.



THE SNAP-CUTANA™ K-METSTAT PANEL comprises 15 DNA-barcoded dNucs carrying disease relevant methyl-lysine PTMs and an unmodified control.

SNAP Spike-ins are useful for:

- In situ validation of antibody specificity
- Monitoring assay performance
- Quantitative sample comparisons
- Troubleshooting experiments



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